AMENDMENTS TO THE SPECIFICATION:

Please amend the paragraph on page 1, lines 15-18 as follows:

In a first aspect the present invention relates to polypeptides having antimicrobial activity, comprising the amino acid sequence, or a fragment thereof of at least 19 amino acids having antimicrobial activity:
G-X_1-X_2-X_3-R-X_4-X_5-X_6-K-I-X_7-X_8-K-X_9-X_{10}-K-X_{11}-X_{12}-X_{13}-X_{14}-I-K-X_{15}-X_{16}-X_{17}-X_{18}-L-V-P (SEQ ID NO: 1);

Please amend the paragraph on page 1, lines 26-35 as follows:

In another aspect the invention relates to polypeptides having antimicrobial activity, comprising an amino acid sequence, which differs by at the most two amino acids from the amino acid sequence:
G-X_1-X_2-X_3-R-X_4-X_5-X_6-K-I-X_7-X_8-K-X_9-X_{10}-K-X_{11}-X_{12}-Z (SEQ ID NO: 1);
wherein
X_1 = L or R; X_2 = L, V, I or F; X_3 = R or K;
X_4 = L, V, I or F; X_5 = R, K, W or G; X_6 = K, R, G, M, N or E;
X_7 = G, R, K or E; X_8 = G, R, K or E; X_9 = L or F;
X_{10} = K or R; X_{11} = I, L, F, C or Y; X_{12} = G, A or T;
Z = R or X_{13}-X_{14}-I-K-X_{15}-X_{16}-X_{17}-X_{18}-L-V-P (SEQ ID NO: 1);

Please amend the paragraph on page 4, lines 1-12 as follows:

Fragment: When used herein, a "fragment" of the amino acid sequence: G-X_1-X_2-X_3-R-X_4-X_5-X_6-K-I-X_7-X_8-K-X_9-X_{10}-K-X_{11}-X_{12}-Z (SEQ ID NO: 1); wherein X_1 = L or R; X_2 = L, V, I or F; X_3 = R or K; X_4 = L, V, I or F; X_5 = R, K, W or G; X_6 = K, R, G, M, N or E; X_7 = G, R, K or E; X_8 = G, R, K or E; X_9 = L or F; X_{10} = K or R; X_{11} = I, L, F, C or Y; X_{12} = G, A or T; Z = R or X_{13}-X_{14}-I-K-X_{15}-X_{16}-X_{17}-X_{18}-L-V-P (SEQ ID NO: 1); wherein X_{13} = Q, L or P; X_{14} = K, I, M, L or V; X_{15} = P, A, H, N or D; X_{16} = I or L; X_{17} = R, H, Q or P; X_{18} = I or K; or anyone of SEQ ID NO:1 to SEQ ID NO:57 or anyone of SEQ ID NO:58 to SEQ ID NO:69 is a subsequence of the polypeptides wherein one or more amino acids have been deleted from the amino and/or carboxyl terminus. Preferably the one or more amino acids have been deleted from the carboxyl terminus. A fragment may consist of at least 19 amino acids, such as 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or 29 amino acids. Preferably a

fragment consists of at least 19 amino acids as counted from the amino terminus of the polypeptide.

Please amend the paragraph on page 5, lines 2-15 as follows:

Modification(s): In the context of the present invention the term "modification(s)" is intended to mean any chemical modification of the polypeptide consisting of the amino acid sequence: G-X_1-X_2-X_3-R-X_4-X_5-X_6-K-I-X_7-X_8-K-X_9-X_{10}-K-X_{11}-X_{12}-Z (SEQ ID NO: 1); wherein X_1 = L or R; X_2 = L, V, I or F; X_3 = R or K; X_4 = L, V, I or F; X_5 = R, K, W or G; X_6 = K, R, G, M, N or E; X_7 = G, R, K or E; X_8 = G, R, K or E; X_9 = L or F; X_{10} = K or R; X_{11} = I, L, F, C or Y; X_{12} = G, A or T; Z = R or X_{13}-X_{14}-I-K-X_{15}-X_{16}-X_{17}-X_{18}-L-V-P (SEQ ID NO: 1); wherein X_{13} = Q, L or P; X_{14} = K, I, M, L or V; X_{15} = P, A, H, N or D; X_{16} = I or L; X_{17} = R, H, Q or P; X_{18} = I or K; or the amino acid sequence shown as amino acids 1 to 29 of anyone of SEQ ID NO:1 to SEQ ID NO:57 or amino acids 1 to 19 of anyone of SEQ ID NO:58 to SEQ ID NO:69 as well as genetic manipulation of the DNA encoding the polypeptides. The modification(s) can be replacement(s) of the amino acid side chain(s), substitution(s), deletion(s) and/or insertions(s) in or at the amino acid(s) of interest; or use of unnatural amino acids with similar characteristics in the amino acid sequence. In particular the modification(s) can be amidations, such as amidation of the C-terminus.

Please amend the paragraph from page 6, line 23 – page 7, line 4 as follows:

In a first aspect, the present invention relates to polypeptides having antimicrobial activity and where the polypeptides comprises, preferably consists of the amino acid sequence: G-X_1-X_2-X_3-R-X_4-X_5-X_6-K-I-X_7-X_8-K-X_9-X_{10}-K-X_{11}-X_{12}-Z (SEQ ID NO: 1);
wherein X_1 = L or R; X_2 = L, V, I or F; X_3 = R or K; X_4 = L, V, I or F; X_5 = R, K, W or G; X_6 = K, R, G, M, N or E; X_7 = G, R, K or E; X_8 = G, R, K or E; X_9 = L or F; X_{10} = K or R; X_{11} = I, L, F, C or Y; X_{12} = G, A or T; Z = R or X_{13}-X_{14}-I-K-X_{15}-X_{16}-X_{17}-X_{18}-L-V-P (SEQ ID NO: 1); wherein X_{13} = Q, L or P; X_{14} = K, I, M, L or V; X_{15} = P, A, H, N or D; X_{16} = I or L; X_{17} = R, H, Q or P; X_{18} = I or K; or amino acids 1 to 29 of anyone of SEQ ID NO:1 to SEQ ID NO:57 or amino acids 1 to 19 of anyone of SEQ ID NO:58 to SEQ ID NO:69. In an interesting embodiment, the amino acid sequence differs by at the most five amino acids (e.g. by five amino acids), such as by at the most four amino acids (e.g. by four amino acids), e.g. by at the most three amino acids (e.g. by three amino acids), particularly by at the most two amino acids (e.g. by two amino acids), such as by one amino acid from the amino acid sequence: G-X_1-X_2-X_3-R-X_4-X_5-X_6-K-I-X_7-X_8-K-X_9-X_{10}-K-X_{11}-X_{12}-Z (SEQ ID NO: 1); wherein X_1

= L or R; X_2 = L, V, I or F; X_3 = R or K; X_4 = L, V, I or F; X_5 = R, K, W or G; X_6 = K, R, G, M, N or E; X_7 = G, R, K or E; X_8 = G, R, K or E; X_9 = L or F; X_{10} = K or R; X_{11} = I, L, F, C or Y; X_{12} = G, A or T; Z = R or X_{13}-X_{14}-I-K-X_{15}-X_{16}-X_{17}-X_{18}-L-V-P (SEQ ID NO: 1); wherein X_{13} = Q, L or P; X_{14} = K, I, M, L or V; X_{15} = P, A, H, N or D; X_{16} = I or L; X_{17} = R, H, Q or P; X_{18} = I or K; or amino acids 1 to 29 of anyone of SEQ ID NO:1 to SEQ ID NO:57 or amino acids 1 to 19 of anyone of SEQ ID NO:58 to SEQ ID NO:69.

Please amend the paragraph from page 7, line 29 – page 8, line 16 as follows:

The polypeptide of the invention may be an artificial variant which comprises, preferably consists of, an amino acid sequence that has at the most three, e.g. at the most two, such as at the most one, substitutions, deletions and/or insertions of amino acids as compared to the amino acid sequence: G-X_1-X_2-X_3-R-X_4-X_5-X_6-K-I-X_7-X_8-K-X_9-X_{10}-K-X_{11}-X_{12}-Z (SEQ ID NO: 1); wherein X_1 = L or R; X_2 = L, V, I or F; X_3 = R or K; X_4 = L, V, I or F; X_5 = R, K, W or G; X_6 = K, R, G, M, N or E; X_7 = G, R, K or E; X_8 = G, R, K or E; X_9 = L or F; X_{10} = K or R; X_{11} = I, L, F, C or Y; X_{12} = G, A or T; Z = R or X_{13}-X_{14}-I-K-X_{15}-X_{16}-X_{17}-X_{18}-L-V-P (SEQ ID NO: 1); wherein X_{13} = Q, L or P; X_{14} = K, I, M, L or V; X_{15} = P, A, H, N or D; X_{16} = I or L; X_{17} = R, H, Q or P; X_{18} = I or K; or amino acids 1 to 29 of anyone of SEQ ID NO:1 to SEQ ID NO:57 or amino acids 1 to 19 of anyone of SEQ ID NO:58 to SEQ ID NO:69. Such artificial variants may be constructed by standard techniques known in the art, such as by site-directed/random mutagenesis of the polypeptide comprising the amino acid sequence shown as the amino acid sequence: G-X_1-X_2-X_3-R-X_4-X_5-X_6-K-I-X_7-X_8-K-X_9-X_{10}-K-X_{11}-X_{12}-Z (SEQ ID NO: 1); wherein X_1 = L or R; X_2 = L, V, I or F; X_3 = R or K; X_4 = L, V, I or F; X_5 = R, K, W or G; X_6 = K, R, G, M, N or E; X_7 = G, R, K or E; X_8 = G, R, K or E; X_9 = L or F; X_{10} = K or R; X_{11} = I, L, F, C or Y; X_{12} = G, A or T; Z = R or X_{13}-X_{14}-I-K-X_{15}-X_{16}-X_{17}-X_{18}-L-V-P (SEQ ID NO: 1); wherein X_{13} = Q, L or P; X_{14} = K, I, M, L or V; X_{15} = P, A, H, N or D; X_{16} = I or L; X_{17} = R, H, Q or P; X_{18} = I or K; or amino acids 1 to 29 of anyone of SEQ ID NO:1 to SEQ ID NO:57 or amino acids 1 to 19 of anyone of SEQ ID NO:58 to SEQ ID NO:69. In one embodiment of the invention, amino acid changes are of a minor nature, that is conservative amino acid substitutions that do not significantly affect the folding and/or activity of the protein; small deletions, typically of one to about 5 amino acids; small amino- or carboxyl-terminal extensions, such as an amino-terminal methionine residue; a small linker peptide of up to about 10-25 residues; or a small extension that facilitates purification by changing net charge or another function, such as a poly-histidine tract, an antigenic epitope or a binding domain.

Please amend the paragraph on page 9, lines 12-21 as follows:

In the context of the invention insertion of a kex2 or kex2-like site result in the possibility to obtain cleavage at a certain position in the N-terminal extension resulting in an antimicrobial polypeptide being extended in comparison to the mature polypeptide shown as the amino acid sequence: G-X_1-X_2-X_3-R-X_4-X_5-X_6-K-I-X_7-X_8-K-X_9-X_{10}-K-X_{11}-X_{12}-Z (SEQ ID NO: 1); wherein X_1 = L or R; X_2 = L, V, I or F; X_3 = R or K; X_4 = L, V, I or F; X_5 = R, K, W or G; X_6 = K, R, G, M, N or E; X_7 = G, R, K or E; X_8 = G, R, K or E; X_9 = L or F; X_{10} = K or R; X_{11} = I, L, F, C or Y; X_{12} = G, A or T; Z = R or X_{13}-X_{14}-I-K-X_{15}-X_{16}-X_{17}-X_{18}-L-V-P (SEQ ID NO: 1); wherein X_{13} = Q, L or P; X_{14} = K, I, M, L or V; X_{15} = P, A, H, N or D; X_{16} = I or L; X_{17} = R, H, Q or P; X_{18} = I or K; or amino acids 1 to 29 of anyone of SEQ ID NO:1 to SEQ ID NO:57 or amino acids 1 to 19 of anyone of SEQ ID NO:58 to SEQ ID NO:69.

Please amend the paragraph on page 10, lines 4-12 as follows:

The present invention also relates to polynucleotides which encode fragments of the amino acid sequence: G-X_1-X_2-X_3-R-X_4-X_5-X_6-K-I-X_7-X_8-K-X_9-X_{10}-K-X_{11}-X_{12}-Z (SEQ ID NO: 1); wherein X_1 = L or R; X_2 = L, V, I or F; X_3 = R or K; X_4 = L, V, I or F; X_5 = R, K, W or G; X_6 = K, R, G, M, N or E; X_7 = G, R, K or E; X_8 = G, R, K or E; X_9 = L or F; X_{10} = K or R; X_{11} = I, L, F, C or Y; X_{12} = G, A or T; Z = R or X_{13}-X_{14}-I-K-X_{15}-X_{16}-X_{17}-X_{18}-L-V-P (SEQ ID NO: 1); wherein X_{13} = Q, L or P; X_{14} = K, I, M, L or V; X_{15} = P, A, H, N or D; X_{16} = I or L; X_{17} = R, H, Q or P; X_{18} = I or K; or anyone of SEQ ID NO:1 to SEQ ID NO:57 or anyone of SEQ ID NO:58 to SEQ ID NO:69 that have antimicrobial activity. A subsequence of the polynucleotides is a nucleotide sequence wherein one or more nucleotides from the 5' and/or 3' end have been deleted.

Please amend the paragraph on page 10, lines 21-32 as follows:

Modification of a nucleotide sequence encoding a polypeptide of the present invention may be necessary for the synthesis of a polypeptide, which comprises an amino acid sequence that has at least one substitution, deletion and/or insertion as compared to the amino acid sequence: G-X_1-X_2-X_3-R-X_4-X_5-X_6-K-I-X_7-X_8-K-X_9-X_{10}-K-X_{11}-X_{12}-Z (SEQ ID NO: 1); wherein X_1 = L or R; X_2 = L, V, I or F; X_3 = R or K; X_4 = L, V, I or F; X_5 = R, K, W or G; X_6 = K, R, G, M, N or E; X_7 = G, R, K or E; X_8 = G, R, K or E; X_9 = L or F; X_{10} = K or R; X_{11} = I, L, F, C or Y; X_{12} = G, A or T; Z = R or X_{13}-X_{14}-I-K-X_{15}-X_{16}-X_{17}-X_{18}-L-V-P (SEQ ID NO: 1); wherein X_{13} = Q, L or P; X_{14} = K, I, M, L or V; X_{15} =

P, A, H, N or D; X_{16} = I or L; X_{17} = R, H, Q or P; X_{18} = I or K; or amino acids 1 to 29 of anyone of SEQ ID NO:1 to SEQ ID NO:57 or amino acids 1 to 19 of anyone of SEQ ID NO:58 to SEQ ID NO:69. These artificial variants may differ in some engineered way from the polypeptide isolated from its native source, *e.g.*, variants that differ in specific activity, thermostability, pH optimum, or the like.

Please amend the paragraph on page 25, lines 26-35 as follows:

The term "effective amount" when used herein is intended to mean an amount of the antimicrobial polypeptide comprising the amino acid sequence: G-X_1-X_2-X_3-R-X_4-X_5-X_6-K-I-X_7-X_8-K-X_9-X_{10}-K-X_{11}-X_{12}-Z (SEQ ID NO: 1); wherein X_1 = L or R; X_2 = L, V, I or F; X_3 = R or K; X_4 = L, V, I or F; X_5 = R, K, W or G; X_6 = K, R, G, M, N or E; X_7 = G, R, K or E; X_8 = G, R, K or E; X_9 = L or F; X_{10} = K or R; X_{11} = I, L, F, C or Y; X_{12} = G, A or T; Z = R or X_{13}-X_{14}-I-K-X_{15}-X_{16}-X_{17}-X_{18}-L-V-P (SEQ ID NO: 1); wherein X_{13} = Q, L or P; X_{14} = K, I, M, L or V; X_{15} = P, A, H, N or D; X_{16} = I or L; X_{17} = R, H, Q or P; X_{18} = I or K; or the amino acid sequence shown as amino acids 1 to 29 of anyone of SEQ ID NO:1 to SEQ ID NO:57 or amino acids 1 to 19 of anyone of SEQ ID NO:58 to SEQ ID NO:69, or a fragment or a variant thereof, which is sufficient to inhibit growth of the microorganisms in question.

Please amend Table 7 on the top of page 47 as follows:

Table 7.

Amino acid sequence	MIC (μg/ml)			
	Micrococcus luteus (ATCC 9341)	*Pseudomonas aeruginosa* (ATCC 27853)	*Escherichia coli* (ATCC10536)	*Klebsiella pneumoniae* (DSM681)
GLLRRLRKKIGKKLKKIGQKIKPIRILVP (SEQ ID NO: 3)	16	4	8	32-64
GLLRRFWKKIGKKLKKFGQKIKPLPKLVP (SEQ ID NO: 41)	32	16	32	32
GLLRRLWRKIGRKLKKYGQKIKALRKLVP (SEQ ID NO: 13)	32	32	64	32
GLLRRLRKKIGKKLKKIAR (SEQ ID NO: 59)	32	8	16	32
GLLKRLGRKIGKKLKKIAR (SEQ ID NO: 66)	64	64	8	Not tested
GLLRRFRKKIGKKLKKIAR (SEQ ID NO: 62)	64	64	16	32-64

Please amend Table 8 on the bottom of page 47 as follows:

Table 8.

Amino acid sequence	MEC (μg/ml)	
	Staphylococcus carnosus	*Escherichia coli* Top10
GLLRRLRKKIGKKLKKIGQKIKPIRILVP (SEQ ID NO: 3)	2.5	8.5
GRIKRVGEKIGKKLKKIGQVIKHLRILVP (SEQ ID NO: 38)	8	8.5
GLLRRFWKKIGKKLKKFGQKIKPLPKLVP (SEQ ID NO: 41)	3.8	16.6
GLLRRLWRKIGRKLKKYGQKIKALRKLVP (SEQ ID NO: 13)	4.4	27.0
GLLRRLRKKIGKKLKKIAR (SEQ ID NO: 59)	1.8	18.3
GLLKRLGRKIGKKLKKIAR (SEQ ID NO: 66)	2	13.5
GLLRRFRKKIGKKLKKIAR (SEQ ID NO: 62)	1.1	28.0